

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 08/910,449A  
Source: 1FW16  
Date Processed by STIC: 8/11/06

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IFW16

## RAW SEQUENCE LISTING

DATE: 08/11/2006

PATENT APPLICATION: US/08/910,449A

TIME: 09:40:45

Input Set : A:\2801-C seq listing.txt

Output Set: N:\CRF4\08112006\H910449A.raw

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3 <110> APPLICANT: Goodwin, Raymond G.
4   Smith, Craig A.
6 <120> TITLE OF INVENTION: 4-1BB Polypeptides and DNA Encoding 4-1BB Polypeptides
8 <130> FILE REFERENCE: 2801-C
10 <140> CURRENT APPLICATION NUMBER: US 08/910,449A
11 <141> CURRENT FILING DATE: 1997-08-05
13 <150> PRIOR APPLICATION NUMBER: US 08/236,918
14 <151> PRIOR FILING DATE: 1994-05-06
16 <150> PRIOR APPLICATION NUMBER: US 08/060,843
17 <151> PRIOR FILING DATE: 1993-05-07
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1254
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus sp.
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (53)..(979)
32 <223> OTHER INFORMATION: (Clone: murine 4-1BB-L)
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36                                     Met Asp
37                                     1
39 cag cac aca ctt gat gtg gag gat acc gcg gat gcc aga cat cca gca      106
40 Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His Pro Ala
41       5                10                15
43 ggt act tcg tgc ccc tcg gat gcg gcg ctc ctc aga gat acc ggg ctc      154
44 Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr Gly Leu
45    20                25                30
47 ctc gcg gac gct gcg ctc ctc tca gat act gtg cgc ccc aca aat gcc      202
48 Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr Asn Ala
49 35                40                45                50
51 gcg ctc ccc acg gat gct gcc tac cct gcg gtt aat gtt cgg gat cgc      250
52 Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg Asp Arg
53       55                60                65
55 gag gcc gcg tgg ccg cct gca ctg aac ttc tgt tcc cgc cac cca aag      298
56 Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His Pro Lys
57    70                75                80
59 ctc tat ggc cta gtc gct ttg gtt ttg ctg ctt ctg atc gcc gcc tgt      346
60 Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Ile Ala Ala Cys
61    85                90                95
63 gtt cct atc ttc acc cgc acc gag cct cgg cca gcg ctc aca atc acc      394

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65      100                      105                      110
67 acc tcg ccc aac ctg ggt acc cga gag aat aat gca gac cag gtc acc      442
68 Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln Val Thr
69 115                      120                      125                      130
71 cct gtt tcc cac att ggc tgc ccc aac act aca caa cag ggc tct cct      490
72 Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly Ser Pro
73      135                      140                      145
75 gtg ttc gcc aag cta ctg gct aaa aac caa gca tcg ttg tgc aat aca      538
76 Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys Asn Thr
77      150                      155                      160
79 act ctg aac tgg cac agc caa gat gga gct ggg agc tca tac cta tct      586
80 Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu Ser
81      165                      170                      175
83 caa ggt ctg agg tac gaa gaa gac aaa aag gag ttg gtg gta gac agt      634
84 Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val Asp Ser
85      180                      185                      190
87 ccc ggg ctc tac tac gta ttt ttg gaa ctg aag ctc agt cca aca ttc      682
88 Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr Phe
89 195                      200                      205                      210
91 aca aac aca ggc cac aag gtg cag ggc tgg gtc tct ctt gtt ttg caa      730
92 Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu Gln
93      215                      220                      225
95 gca aag cct cag gta gat gac ttt gac aac ttg gcc ctg aca gtg gaa      778
96 Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val Glu
97      230                      235                      240
99 ctg ttc cct tgc tcc atg gag aac aag tta gtg gac cgt tcc tgg agt      826
100 Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp Ser
101      245                      250                      255
103 caa ctg ttg ctc ctg aag gct ggc cac cgc ctc agt gtg ggt ctg agg      874
104 Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu Arg
105      260                      265                      270
107 gct tat ctg cat gga gcc cag gat gca tac aga gac tgg gag ctg tct      922
108 Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu Ser
109 275                      280                      285                      290
111 tat ccc aac acc acc agc ttt gga ctc ttt ctt gtg aaa ccc gac aac      970
112 Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp Asn
113      295                      300                      305
115 cca tgg gaa tgagaactat ccttcttggtg actcctagtt gctaagtcct      1019
116 Pro Trp Glu
119 caagctgcta tgttttatgg ggtctgagca ggggtccctt ccatgacttt ctcttgctctt      1079
121 taactggact tggatattat tctgagcata gctcagacaa gactttatat aattcactag      1139
123 atagcattag taaactgctg ggcagctgct agataaaaaa aaatttctaa atcaaagttt      1199
125 atatttatat taatatataa aaataaatgt gtttgtaaata aaaaaaaaaa aaaaa      1254
128 <210> SEQ ID NO: 2
129 <211> LENGTH: 309
130 <212> TYPE: PRT
131 <213> ORGANISM: Mus sp.
133 <400> SEQUENCE: 2

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135 Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His
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139 Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr
140          20          25          30
143 Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr
144          35          40          45
147 Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg
148          50          55          60
151 Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His
152 65          70          75          80
155 Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Ile Ala
156          85          90          95
159 Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr
160          100         105         110
163 Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln
164          115         120         125
167 Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly
168          130         135         140
171 Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys
172 145          150         155         160
175 Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr
176          165         170         175
179 Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val
180          180         185         190
183 Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro
184          195         200         205
187 Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val
188          210         215         220
191 Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr
192 225          230         235         240
195 Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser
196          245         250         255
199 Trp Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly
200          260         265         270
203 Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu
204          275         280         285
207 Leu Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro
208          290         295         300
211 Asp Asn Pro Trp Glu
212 305

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215 &lt;210&gt; SEQ ID NO: 3

216 &lt;211&gt; LENGTH: 1618

217 &lt;212&gt; TYPE: DNA

218 &lt;213&gt; ORGANISM: Homo sapiens

221 &lt;220&gt; FEATURE:

222 &lt;221&gt; NAME/KEY: CDS

223 &lt;222&gt; LOCATION: (4)..(765)

224 &lt;223&gt; OTHER INFORMATION: (clone: human 4-1BB-L (7A)

226 &lt;400&gt; SEQUENCE: 3

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227	gtc	atg	gaa	tac	gcc	tct	gac	gct	tca	ctg	gac	ccc	gaa	gcc	ccg	tgg	48
228		Met	Glu	Tyr	Ala	Ser	Asp	Ala	Ser	Leu	Asp	Pro	Glu	Ala	Pro	Trp	
229	1					5					10					15	
231	cct	ccc	gcg	ccc	cgc	gct	cgc	gcc	tgc	cgc	gta	ctg	cct	tgg	gcc	ctg	96
232	Pro	Pro	Ala	Pro	Arg	Ala	Arg	Ala	Cys	Arg	Val	Leu	Pro	Trp	Ala	Leu	
233					20					25					30		
235	gtc	gcg	ggg	ctg	ctg	ctg	ctg	ctg	ctc	gct	gcc	gcc	tgc	gcc	gtc		144
236	Val	Ala	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Cys	Ala	Val		
237				35					40				45				
239	ttc	ctc	gcc	tgc	ccc	tgg	gcc	gtg	tcc	ggg	gct	cgc	gcc	tcg	ccc	ggc	192
240	Phe	Leu	Ala	Cys	Pro	Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly	
241			50					55					60				
243	tcc	gcg	gcc	agc	ccg	aga	ctc	cgc	gag	ggt	ccc	gag	ctt	tcg	ccc	gac	240
244	Ser	Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	
245		65				70					75						
247	gat	ccc	gcc	ggc	ctc	ttg	gac	ctg	cgg	cag	ggc	atg	ttt	gcg	cag	ctg	288
248	Asp	Pro	Ala	Gly	Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu	
249	80					85					90					95	
251	gtg	gcc	caa	aat	gtt	ctg	ctg	atc	gat	ggg	ccc	ctg	agc	tgg	tac	agt	336
252	Val	Ala	Gln	Asn	Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser	
253				100						105					110		
255	gac	cca	ggc	ctg	gca	ggc	gtg	tcc	ctg	acg	ggg	ggc	ctg	agc	tac	aaa	384
256	Asp	Pro	Gly	Leu	Ala	Gly	Val	Ser	Leu	Thr	Gly	Gly	Leu	Ser	Tyr	Lys	
257				115						120					125		
259	gag	gac	acg	aag	gag	ctg	gtg	gtg	gcc	aag	gct	gga	gtc	tac	tat	gtc	432
260	Glu	Asp	Thr	Lys	Glu	Leu	Val	Val	Ala	Lys	Ala	Gly	Val	Tyr	Tyr	Val	
261				130						135					140		
263	ttc	ttt	caa	cta	gag	ctg	cgc	gtg	gtg	gcc	ggc	gag	ggc	tca	ggc		480
264	Phe	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	
265			145				150					155					
267	tcc	gtt	tca	ctt	gcg	ctg	cac	ctg	cag	cca	ctg	cgc	tct	gct	gct	ggg	528
268	Ser	Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly	
269	160					165					170					175	
271	gcc	gcc	gcc	ctg	gct	ttg	acc	gtg	gac	ctg	cca	ccc	gcc	tcc	tcc	gag	576
272	Ala	Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu	
273					180					185						190	
275	gct	cgg	aac	tcg	gcc	ttc	ggt	ttc	cag	ggc	cgc	ttg	ctg	cac	ctg	agt	624
276	Ala	Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser	
277				195						200					205		
279	gcc	ggc	cag	cgc	ctg	ggc	gtc	cat	ctt	cac	act	gag	gcc	agg	gca	cgc	672
280	Ala	Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg	
281			210					215							220		
283	cat	gcc	tgg	cag	ctt	acc	cag	ggc	gcc	aca	gtc	ttg	gga	ctc	ttc	cgg	720
284	His	Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg	
285		225					230					235					
287	gtg	acc	ccc	gaa	atc	cca	gcc	gga	ctc	cct	tca	ccg	agg	tcg	gaa		765
288	Val	Thr	Pro	Glu	Ile	Pro	Ala	Gly	Leu	Pro	Ser	Pro	Arg	Ser	Glu		
289	240					245						250					
291	aacgcccagc	ctgggtgcag	cccacctgga	cagagtcgga	atcctactcc	atccttcatg											825

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297 atatttattc tgagcctgag ctcagataat atattatata tattatata atatatatat    1005
299 ttctatttaa agaggatcct gagtttgtga atggactttt ttagaggagt tgttttgggg    1065
301 ggggggtctt cgacattgcc gaggctgggtc ttgaactcct ggacttagac gatcctcctg    1125
303 cctcagcctc ccaagcaact gggattcatc ctttctatta attcattgta cttatttgcc    1185
305 tatttggtgtg tattgagcat ctgtaatgtg ccagcattgt gccaggcta gggggctata    1245
307 gaaacatcta gaaatagact gaaagaaaat ctgagttatg gtaatacgtg aggaatttaa    1305
309 agactcatcc ccagcctcca cctcctgtgt gatacttggg ggctagcttt tttctttctt    1365
311 tctttttttt gagatgggtc tgttctgtca accaggctag aatgcagcgg tgcaatcatg    1425
313 agtcaatgca gcctccagcc tcgacctccc gaggctcagg tgatcctccc atctcagcct    1485
315 ctcgagtagc tgggaccaca gttgtgtgcc accacacttg gctaactttt taattttttt    1545
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322 <210> SEQ ID NO: 4
323 <211> LENGTH: 254
324 <212> TYPE: PRT
325 <213> ORGANISM: Homo sapiens
327 <400> SEQUENCE: 4
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337 Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
338          35          40          45
341 Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser
342          50          55          60
345 Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
346 65          70          75          80
349 Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
350          85          90          95
353 Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
354          100         105         110
357 Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
358          115         120         125
361 Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
362          130         135         140
365 Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
366 145          150         155         160
369 Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
370          165         170         175
373 Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
374          180         185         190
377 Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
378          195         200         205
381 Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
382          210         215         220
385 Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
386 225          230         235         240

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VERIFICATION SUMMARY

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